

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 7, 2002, 19:53:06 ; Search time 3270.98 Seconds  
(without alignments)  
11291.826 Million cell updates/sec

Title: US-09-993-874-1

Perfect score: 1765  
Sequence: 1 tcagtgcaagactttagga.....aaaaaaaaaaaaaaaa 1765

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	1763.4	99.9	1765	3	AF139644	AF139644 Phrixothr
2	1284.4	72.8	1760	3	AF139645	AF139645 Phrixothr
3	582	33.0	1659	6	I40164	I40164 Sequence 1
4	581.6	33.0	1647	3	AF328553	AF328553 Pyrococell
5	581.4	32.9	1659	6	I40165	I40165 Sequence 2
6	580.6	32.9	1922	3	PIBLUCIF	L39928 Pyrococella
7	580.4	32.9	1725	3	LNLUCPROT	X89479 L.noctiluca
8	577	32.7	1831	3	PPU31240	U31240 Photuris pe
9	575.2	32.6	2193	6	AX074306	AX074306 Sequence
C 10	575.2	32.6	2193	6	AX074308	AX074308 Sequence
C 11	575.2	32.6	2268	6	AX074303	AX074303 Sequence
C 12	575.2	32.6	2268	6	AX074305	AX074305 Sequence
C 13	573.8	32.5	1638	6	AX074300	AX074300 Sequence
C 14	573.8	32.5	1638	6	AX074302	AX074302 Sequence
15	571.6	32.4	1642	6	AX098293	AX098293 Sequence
16	566.8	32.1	1639	6	AX098286	AX098286 Sequence
17	565.2	32.0	1639	6	AX098283	AX098283 Sequence
18	565.2	32.0	1639	6	AX098284	AX098284 Sequence
19	563.6	31.9	1639	6	AX098285	AX098285 Sequence
20	560.4	31.8	1639	6	AX098282	AX098282 Sequence
21	560.4	31.8	1639	6	AX098292	AX098292 Sequence
22	559.2	31.7	1639	6	AX098288	AX098288 Sequence
23	558.8	31.7	1639	6	AX098323	AX098323 Sequence
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25	556	31.5	1639	6	AX098291	AX098291 Sequence
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27	554.4	31.4	5620	6	AR091518	AR091518 Sequence
28	554.4	31.4	5620	6	AR154398	AR154398 Sequence
29	554.4	31.4	5620	6	AR174326	AR174326 Sequence
30	554.4	31.4	5620	6	AX080362	AX080362 Sequence
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32	552.8	31.3	1811	6	A37556	A37556 Sequence 22
33	552.8	31.3	4672	12	CVE277960	AJ277960 Cloning v
34	552.8	31.3	4674	12	XX002437	U02437 Cloning vec
35	552.8	31.3	5067	12	AF093685	AF093685 Luciferas
36	552.8	31.3	5499	12	AF093684	AF093684 Luciferas
37	552.8	31.3	5596	12	CVLUCLIC	U25266 Ligation-in
38	552.8	31.3	5597	12	CVPGL2BAS	X65323 Cloning vec
39	552.8	31.3	5675	12	AF053698	AF053698 Reporter
40	552.8	31.3	5688	12	AF053461	AF053461 Reporter
41	552.8	31.3	5695	12	AF053315	AF053315 Reporter
42	552.8	31.3	5714	12	AF167311	AF167311 Reporter
43	552.8	31.3	5743	12	AF053462	AF053462 Reporter
44	552.8	31.3	5748	12	AF058756	AF058756 Cloning v
45	552.8	31.3	5789	12	CVPGL2PRO	X65326 Cloning vec

ALIGNMENTS

RESULT 1	AF139644	1765 bp	MRNA	linear	INV 14-DEC-1999
LOCUS	AF139644				
DEFINITION	Phrixothrix vivianli				
ACCESSION	AF139644				
VERSION	AF139644.1	GI:4959884			
KEYWORDS					
SOURCE	Phrixothrix vivianli.				
ORGANISM	Phrixothrix vivianli.				
REFERENCE					
AUTHORS	Viviani,V.R., Bechara,E.J. and Ohmliya,Y.				
TITLE	Cloning, sequence analysis, and expression of active Phrixothrix				
	railroad-worms luciferases: relationship between bioluminescence				
	spectra and primary structures				
JOURNAL	Biochemistry 38 (26), 8271-8279 (1999)				
MEDLINE	99315203				
PUBMED	10387072				
REFERENCE	2 (bases 1 to 1765)				
AUTHORS	Viviani,V.R. and Ohmliya,Y.				
TITLE	Direct Submission				

JOURNAL Submitted (31-MAR-1999) Biochemistry, Shizuoka University, 836,  
Oya, Shizuoka 422, Japan  
FEATURES Location/Qualifiers  
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BASE COUNT 594 a 316 c 348 g 507 t  
ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1764; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tcagtgcaagactttaggatcaaaaatggaagaacaattaggcatgagagcgctcc 60  
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QY 61 tcgtgatagtccatcctgctgcgcaggaacaacattataccaatcattgataaatt 120  
Db 61 TCGTGAATAGTCCATCCTGGCTCGGCAGACAACAATATTACCAATCATGTATAAATT 120  
QY 121 tgcattcttccttgaagcaataatcgatgctacatacaatgaatgaatataatgctca 180  
Db 121 TGCATCTTTTCTTGAGCAATTAATGCATGCTACAAATGAAGTAATATCATATGCTCA 180  
QY 181 aatattgaaaccagctgcgcgttagctgttagtatagaacaataatgcttgaatgaaa 240  
Db 181 AATATTGAAACCAGCTGCGCCTTAGCTGTAGTATGAGAACATATATGCGTTGAATGAAAA 240  
QY 241 caatgttgggtgtatgcagtgaaaaacaataaacttttaatccttgcctgtctgc 300  
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QY 301 ttatacttaggaataccagtagcaacatcaaatgatatgtacacagatggaagttaac 360  
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QY 1741 aaaaaaaaaaaaaaaaaa 1765  
Db 1741 AAAAAAAAAAAAAAAAAA 1765

RESULT 2  
AF139645 1760 bp mRNA linear INV 14-DEC-1999  
LOCUS Phrixothrix hirtus red-bioluminescence eliciting luciferase mRNA,  
DEFINITION complete cds.  
ACCESSION AF139645  
VERSION AF139645.1 GI:4959886  
KEYWORDS  
SOURCE Phrixothrix hirtus.  
Phrixothrix hirtus.  
Phrixothrix hirtus  
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
Elateriformia; Cantharoidae; Phengodidae; Phrixothrix.  
REFERENCE  
AUTHORS 1 (bases 1 to 1760)  
TITLE Viviani,V.R., Bechara,E.J. and Ohmiya,Y.  
JOURNAL Cloning, sequence analysis, and expression of active Phrixothrix  
MEDLINE railroad-worms luciferases: relationship between bioluminescence  
PUBMED spectra and primary structures  
99315203 Biochemistry 38 (26), 8271-8279 (1999)  
10387072

REFERENCE  
AUTHORS 2 (bases 1 to 1760)  
TITLE Viviani,V.R. and Ohmiya,Y.  
JOURNAL Direct Submission  
Submitted (31-MAR-1999) Biochemistry, Shizuoka University, 836,  
Oya, Shizuoka 422, Japan  
FEATURES  
source location/Qualifiers  
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ORIGIN

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Best Local Similarity 84.9%; Pred. No. 9.9e-256;  
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QY 73 ccatacctgcgtcgcagagacaacaatatataccaatcatgtataaatttgcatctttcc 132  
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QY 133 tgaagcaataatcgatgctcatatacaaatggaagtaataatcatatgctcaaatattggaac 192  
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QY 373 tatacaaaaccaatcatcatgtttagttcaagaagaagcaactccgcgtatcttgagagt 432  
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Db 1048 ATATGGATTAAACCGAAACCTGCAGCGCTCTAATACTTAGCCCCAATGATCGAAGACTTAA 1107  
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Db	1348	GAAAGAACCTATTAAATATAAAGGATATCAGGTGGCGCTGCTGAAC TGAAAAATCTGCT	1407
QY	1390	tttacaacatccaagtattgctgatgcyggigtactggaqtccggaacnatttgtg	1449
Db	1408	TTTACAACATCCAATATTTCGTGATCGGGTGTTA-TTGAATCCGGACGAATTTCGTGG	1466
QY	1450	acaatlacc-tgctgtcgttgtgtgttagaatctgycgaagcgcgtgactgtaaaagya	1508
Db	1467	TCAATTACCCTTTCGCGTGTGTGTGTAGAGCCTGGTAAGACAATGACCGAALAAGAAG	1526
QY	1509	ttcaagatttatttgcagcacaaagtcactccaacaagcatcttcgagcggtgtcgtat	1568
Db	1527	TTCAGGATTATATTGCAGAGCTAGTCACTACACTAAACATCTTCGAGCGGTCGTAT	1586
QY	1569	ttgtagacaglatccgaaagccctacttgyaaaaactcagaaatcagaagaagctccyagaa	1628
Db	1587	TTATAGATAGTATTTCCAAAAGGCCCAACAGGAAACCTCATGAGAAACGAACCTCCGAGCAA	1646
QY	1629	tattgcccagcgagcacccaataatcaaaaattataaagttccaatgttatgtcttaagttcta	1688
Db	1647	TATTTGCCCGGGAACAGGCAAAATCAAAATTTATAAGCTCAATATATTTGCTTAGTTATTA	1706
QY	1689	aatgtatataaacaaagttttlagaacctaatatcatctcaataactaacaana	1742
Db	1707	AATGTATGTATCAAAATTTTGAACCTTAATACATTCATTGAGAGCCTAAAAAAA	1760

RESULT	3			
LOCUS	I40164			
DEFINITION	I40164	1659 bp	DNA	
ACCESSION	I40164	Sequence 1 from patent US 5618722.		linear
VERSION	I40164.1	GI:2083169		PAT 13-MAY-1997
KEYWORDS				
SOURCE		Unknown.		
ORGANISM		Unknown.		
REFERENCE		Unclassified.		
AUTHORS		1 (bases 1 to 1659)		
TITLE		Zenko,S., Shiraiishi,S., Inouye,S. and Saigo,K.		
JOURNAL		Photuris firefly luciferase gene		
FEATURES		Patent: US 5618722-A 1 08-APR-1997;		
source		Location/Qualifiers		
		1..1659		

BASE COUNT	ORIGIN	/organism="unknown"
321 a	193 c	265 t
		268 g
		612 others

Query Match	33.0%;	Score 582;	DB 6;	Length 1659;
Best Local Similarity	43.6%;	Pred. No. 2e-110;		
Matches 704;	Conservative 247;	Mismatches 655;	Indels 9;	Gaps 2;

QY	31	agaagaaaacatttaggcattggaagcgtcctcgtgatatagtcacatccctgctcgacag	90
		:  :     : : :       :  :	
Db	9	HGARAAYAAAYATHYTNATHGNCNCNCNCNTAYATYCCNYTNGARGARGENACNGCNG	68
QY	91	acaacaattataccaatcatctgfatataatttgcacbtcttcctgaagcaata-----at	144
		: : :   ::     :     :	
Db	69	NGARCARYTNCAVYMGNGCNATHCNMGNTAYGCGNCNGTNCNGNACNYTNGCNTAYAC	128
QY	145	cgatgctcatacaatggaagtatatcatatgctcaaatatttgaaccagctgcgcgt	204
		:    : :	
Db	129	NGAYGTNCAYACNGARYTNGARGTNACNTAYAARGARTTYTNGAYGTNACNTGYCGCYT	188
QY	205	agctgtgatatagaacaatatgcttgaatgaaaaacaatgttgtggtgtatgcattga	264
Db	189	NGCNGARGCNCATGARAAYATYAGNYTNGGNYTNCARCAYACNATHCNGTNTGYTCNGA	248
QY	265	aaacaataaactttttaaactcgtcccttgcctgcttataacttaggaataaccagtagc	324
		:  :         : :      :       :	

Db	249	RAAYTGyTNCARtTtTtYATGCCNATHtTGcNGcNcYtNTAYtNGNGtNGcNACNGC	308
QY	325	aacatcaaatlgatatgtacacagatggaagttaaactggtcatttgaatatatacaaac	384
Db	309	NCCNACNAAYGAYtHTtAYAAyGARMGNGARyTNTAYAAyTCNTtNCNATHtCNCARCC	368
QY	385	aactatcatgtttagtttcaaagaagaagcattcccgcttattctgagagtacagcaaatct	444
Db	369	MACNGTNGTtNTtYACNTtCNMGNAAYtCYNTNCARARATHtYtNGNGtNCARTcNMGNtT	428
QY	445	aagttcatataaaaaagtcgtagttlatcgaatagcatgttgcagcaattaatgycgttgaatg	504
Db	429	NCCNATHATHAARAARATHATHATHtYtNGAYcGNAARAARARGAYtAYtTNGGNTAYcARTc	488
QY	505	cgtatctaccttgttgcacgltatactgaaccacacacttgaatccattgtcattacaac	564
Db	489	NATGCARTcNTtYATGAARGARCAYGTNCcNGcNAAYtTYAAyGTNTcNGcNTtYARCC	548
QY	565	aaaagatttgaatccccccttgaaaaaacgcattaatatgtcatcatctggaacaactg	624
Db	549	NYTNTcNTtTGA---YtTNGAYMGNGtNGcNTGYATHATGAAYtCtNCtNGcNTcNACNGG	605
QY	625	atgccaagaaggtgtagttactgagccatagaaagtctaactataagaattcgttcaatagcag	684
Db	606	NYTNCcNAARGNGtNCcNATHtCNCAYMGNAAYACNAITHtAYMGNTtYtCNCAYtGYMG	665
QY	685	ggatcccaattatgycactcgtgaaggttccacaacaatcaattcttccttagtaccgtt	744
Db	666	NGAYCCNGtNTtYcGNAAYCARATHATHCCNGAYACNACNATHtYtNTGYcGcNGtNCcNTT	725

QY	745	ccatcatgccttctggaaatgcttactacattatcttactctgtagtaggaactaaagttgt	804
Db	726	ycaycaygcnttytggnacnttyaacnaayttingntatytathtgyggnttycaygtngt	785
QY	805	aatgttgaagaataatttgaagggcgacttctctlaaaaaacatacagaattccaaaatccc	864
Db	786	nytnatgtaymgnttyaaygarcaaytnttytncaracnnytnccargaytayaartgyca	845
QY	865	cactattgtagtyggccctccagtltagtgttcttggctaaagcccatagtcgatca	924
Db	846	rtcngcnytnytnngtncnacngntnytnngcnttytngcnaaraayccnytnngtngayaa	905
QY	925	atacgattatcgagcttaacgyaaagttgctactgaggyagctcccttaggaaaagatgt	984
Db	906	rtaygaytntncnaayytncaaygarathgcntcngcngngcncnytnncnaaragarat	965
QY	985	cgcgaagcagtagcaagaaggttgaaatctaccgtgaatcatatacaagatatgattaac	1044
Db	966	htcngarathgcnccnaarbgnttyaarytnccngcnathmgncargntayggnytnc	1025
QY	1045	tgaacttgcctgcgtgctgaatgattaccctcataatgctgttgaaaaaagttcactg	1104
Db	1026	ngaracnacntgygcnaathgtnathacngcngarbgngarttyaarytnngcngcngtng	1085
QY	1105	aagacccttgcacatatcaataagctaaagtttagataacgctactgyggaagcgctag	1164
Db	1086	naargtngtncnttytatytcntynaargtntngayytmaayacngcnaraarytng	1145
QY	1165	accagggaaagagcggaataatgcttccaagtgaatgatatgataaagataatacaa	1224
Db	1146	nccnaaygarcmgngcngarathtgyttyaargngccnatgatthtgaarbgntayathaa	1205
QY	1225	caatccggaagcaactattgatactatgaacaaagatggttgcctcatctctgagatat	1284
Db	1206	yaayccngarcmcnacngcgantynatthgaygarbgngtgatthcaytccngngayatt	1265
QY	1285	tgatatattacgaagaaagatgtaaatcttcttatagttgatcgatgtaagaactatcaa	1344
Db	1266	hgcntayttygaygargayggncaygtntayathtgtngaymgntynaartcnytnatthaa	1325
QY	1345	atacaagggatatacaggttgcgcctctgtaaacctggaataatctgcttaccacatccaag	1404
Db	1326	rtayaaarggnatycargtncnccngcngaryytnrgargcnytnytnccarcaycwnyt	1385

[illegible]

RESULT	4
AF328553	
LOCUS	AF328553
DEFINITION	Pyrocoel1a rufa luciferase mRNA, complete cds.
ACCESSION	AF328553
VERSION	AF328553.1
	GI:12018177
	1647 bp
	mRNA
	linear
	INV 17-DEC-2001

**SOURCE ORGANISM**

מבוא

**AUTHORS** Lee, K.S., Park, H.J., Bae, J.S., Goo, T.W., Kim, I., Sohn, H.D. and

TITLE	Molecular cloning and expression of a cDNA encoding the luciferase from the firefly, <i>Pyrocoelia rufa</i>
JOURNAL	J. Biotechnol. 92 (1), 9-19 (2001)

PUBMED 11604168

AUTHORS      Lee, K.S., Park, H.J.,

**JOURNAL Submitted (12-DEC-2000) Laboratory of Genetic Engineering of**

Dong-A University, 840 Hadan 2 dong, Sahagu, Pusan 604-714, Korea

Source

CDS

BASE COUNT	ORIGIN
516 a	287 c
	358 g
	486 t

Query Match	33.0%;	Score 581.6;	DB 3;	Length 1647;
Best Local Similarity	60.6%;	Pred. No. 2.4e-110;		
Matches 991; Conservative	0;	Mismatches 634;	Indels 9;	Gaps 2;

QY 36 aaacattagcgtgagagcgtcctcgtgatatagtccatcctgctcgagacaac 95

[illegible]

QY 330 caatgatatgtcacagatgagagtttaactgtcatttgaatatatcaaaaccaacta 389  
 ||||| |||| | | | | | |||| | |||| | |||| | |||| |  
 Db 317 CAATGATATTTACATGAACGTGAATTTACACACAGTTTGTTCATATCACAACCTACAA 376

QY 390 tcatgtttagttcaagaagcactccgccttattctgaggtacagcaaatctaagtt 449

Db 377 TAGTATTTTGTCTAAAGAGCGCTCCAAAATCCTAGGAGTACATAAGAAATTACCTG 436

450 tcattaaaagtcgtagtatcgtatagcatgtacgacattaatggcgttgaaatgcgtat 509

Db 437 TCATTCAAAAATTGTTATTCTGGATTCTCGAGAGGATTATATGGGAACAATCTATGT 496

QY 510 ctaccttgtgcacgttatactgaccacaccttgatcatgtcatcttacaccaaaag 569

Db 497 ACTCGTTCATTGCAATCACATCTACCTGCAGGTTTTTAATGAATATGATTACATACCGGATT 556

QY 570 atttgatcccttgaaaaatcgcatataatgtcatcatctggaacaactgattgc 629

Db 557 CTTTGACCGGGAACAGCAGCACTTATATGATTCTATCGGATCTACTGGATTAC 616

630 ctaagggtgtagtactgagccatagaagtctaactataagatctggtcatagcaggatc 689

Db 617 CCAAGGAGTTGATCTTACTCACATGATGTTTGTGTTAGATTTCTCTCACTGCAGAGATC 676

QY 690 ccattatgcactcgtacggtccacaacatcaattcttcttagtaccggtccatc 749

Db 677 CTGTGTTGGTAATCAATTAATCCCGATACTGGGATTTAACAGTTATACCATTTTCATC 736

QY 750 atgccttggaaatgttactacattatcttacttggtagtagacttaagttgtaatgt 809

Db 737 ATGGTTTGGAAATGTTTACAACATTAGGATATTTAACGTGTGGAATTCGTATTGTCCTTA 796

QY 810 tgaagaaatttgaqqccacttttcttaaaaaaccatacacaaattacaanaatcccacta 869

Db 797 TGTATGATTTGAGAGGAATTTTACGATCCCTTCAAGATTATAAATTCAAGTG 856

Qy 870 ttgtatqgccccctccaattatqgtatttttqgctaanaaqqccattatgcatacaatcacg 929

Db 857 CGTTGCTGTACCTACCCCTATTTCATTCTTTGCCAAAGCACATTAGTCGACAATACG 916

QY 930 atttatcgaqcttaacqgaatttqctacttqqaqaqctccttlaqgaaaaaqaatgttcqcaq 989

Db 917 ATTTATCCACTTACATGAATTGCTTCCGGTGGAGCTCCTCTCGCGAAGAAGTTGGAG 976

Ov 990 aaqcaqtaccaaqaqqttaaaattacctqqaatcatacaaqaatatqatlaactqaaa 104

Db 977 AAGCGTAGCAAAACGTTTAAAGTTGCCGGCATACGACAAGGGACGACTTACCGAA 103

0y 1050 cttgctgcgcctgtaatgattacccctcataatgctctgtqaaaaacaagttcaacttqgaagac 110

Db 1037 CTACCTCAGCTATTATTAATTACACCAGAAGGGGATGATAAACCGGAGCATGTGGTAAG 109

Ov 1110 ccttccatacatltaaaqctaqaattttaqataaacqctacttqqaaqccqctaqaaccaq 116



Db 1097 TCGTTCATTCCTTGCGGCCCAAATTTGTGATCTGGATACGGGCAAAACTTTGGGGTTA 1156  
QY 1170 gagaaagcggaatatgcttcaaagtgaatgattatgaagatatlacacaatc 1229  
Db 1157 ATCAGAGAGGGGAATTATGTGTGAAGGTCCAATGATGAAGGCTTACGTAACCAACC 1216  
QY 1230 cggaaagcaactatgatactattgacaaaagatggtgtgcttcattctgagatatgtat 1289  
Db 1217 CAGAAGCAACAAATGCATTGATAGCAAAAGATGATGGTTACACTCTGTGATATAGCTT 1276  
QY 1290 attacgacgaagtgaatcttctatatagttgattgattgaaagaacttattaataca 1349  
Db 1277 ACTATGACAAAGATGCTCACTTCTCATAGTGATCGTGTGAATCGTTAATTAATACA 1336  
QY 1350 agggatatacaggttgcgcctgtcgaactggaataatctgcttltacaacatccaagtattg 1409  
Db 1337 AAGGTATACAGGTACCGCCTGCCGAATTAGATCGATATTGTTACAACATCCCTTCATAT 1396  
QY 1410 ctgatgcggtgttactggaagttcccgagcaaatgtgtgagacaattacctgctgtgtg 1469  
Db 1397 TTGATGCAGGTGTTCAGGAATTCGCCGATCCAGATGCCGGTGAACCTTCGACGCCGTTG 1456  
QY 1470 ttgtttagaatctgcaagaagcgtgactgaaagaagtccaagatttattgcaagcac 1529  
Db 1457 TTGCTTTAGAGCAAGCGCAAAATGATGACCGAACAGAGAGTGTGATTACGTTGCGGGAC 1516  
QY 1530 aagtcactccaacaaagcatcttcgaagcggtgtcgttattgtagacagttaccgaag 1589  
Db 1517 AAGTAACCTGCTTCTAAGCGTTTACGTGAGAGATTAACTTTGTGACGAAAGTACCAAAAG 1576  
QY 1590 gccctactggaaaactcatcagaagaagagctccgagaataattgcccagcgagcacc 1649  
Db 1577 GTCTAACTGGAAAGATTGATTCAGAAATAATTAGGAGATCCTTACAATG---GGACAAA 1633  
QY 1650 aatcaaaaattataa 1663  
Db 1634 AATCCAAATTGTAA 1647

RESULT 5  
LOCUS 140165 1659 bp DNA linear PAT 13-MAY-1997  
DEFINITION Sequence 2 from patent US 5618722.  
ACCESSION 140165  
VERSION 140165.1 GI:2083170  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1659)  
AUTHORS Zenno,S., Shiraishi,S., Inouye,S. and Saigo,K.  
TITLE Photurins firefly luciferase gene.  
JOURNAL Patent: US 5618722-A 2 08-APR-1997;  
FEATURES  
source location/Qualifiers  
1. 1659  
BASE COUNT 321 a 193 c 268 g 265 t 612 others  
ORIGIN

Query Match 32.9%; Score 581.4; DB 6; Length 1659;  
Best Local Similarity 43.6%; Pred. No. 2.6e-110;  
Matches 704; Conservative 247; Mismatches 655; Indels 9; Gaps 2;

QY 31 agaagaaacattagcgatgagagcgtcctcgtgatatagttccatcctggtcgcgaag 90  
Db 9 HGARAAAYAAAYATHTNATHGNCNCNCNCNTAYTAYCCNNTNGARGARGNACNGCNGG 68  
QY 91 acaacaattataccaatcattgtataaatttgcatcttctcctgaaagcaata-----at 144  
Db 69 NGARCARYTNCAVWNGCNATHHTCNMGNTAYGCGNGCNGTNCNGNACNYTNGCNTAYAC 128  
QY 145 cgatgctcatacaaatgaagtaatatatgctcaaatatttgaaacagctgcgcgtt 204

Db 129 NGAYGTMCAYACNGARYTNGARGTNACNTAYAAARGARTTYTNGAYGTNACNTGYCCYT 188  
QY 205 agctgttagtatagaacaatatgcttgaatgaaacaatgtgtgtgtatgcaagtga 264  
Db 189 NGCNGARGCNATGAARAAAYTAYGNYTNGNYTNCARCAVACNATHHTCNMTNGTYCNGA 248  
QY 265 aaacaataaactttttaatccctgtccctgtcgtccttatacttagaataaccagtagc 324  
Db 249 RAAVGTGTNCARTTYTAYTGCCNATHGTGYCNGCNYTNTAYGTNGCNGTNCNACNGC 308  
QY 325 aacatcaaatgatatgtacacagatgagagtttaactggtcatttgaatatacaacc 384  
Db 309 NCCNACNAAYGAYATHYTAAYGARMGNGARYTNTAYAYTCNNTNTHCNATHHTCNARCC 368  
QY 385 aactatcatgtttagttcaagaagaagcactccgccttattctgagagtacagcaaatct 444  
Db 369 NACNGTNGTNTTYACNTCMGNAAAYTCNNTNCARARATHYTNNGNGTNCARTCMGNYT 428  
QY 445 aagttcaataaaaagtcgtagttatcgatagcatgtacgacatlaatgycgttgaatg 504  
Db 429 NCCNATHATHAARAARATHATHYTNAGYGNAAARAARGAYTAYTNGNTAYCARTC 488  
QY 505 cgtatctaccttgttgcaagcttatactgacacacaccttgcattgcatttacacc 564  
Db 489 NATGCARTCNTTYATGAARGARCAVGTNCCNGCNAAYTYAAYGTNTCNGCNTTYAARCC 548  
QY 565 aaaagatttgatcccttgaaaaaatcgcatlaattatgtcatcatctggaacaactyg 624  
Db 549 NYTNTCNTTYGA---YTNAGAYMNGTNGCNTGYATHATGAAYTCNTCNGNTCMACNGG 605  
QY 625 atgcctaaggtgtgtagttactgagccatagaagttcaactataagattcgttcataag 684  
Db 606 NYTNCNAAARGGNTNCCNATHHTCNCAVGMNAAYACNATHYVMGNTTYTCNCAIYGYMG 665  
QY 685 ggtatccattatgagcaactcgtacggttccacaacaatcaatcttccctagtagcgtt 744  
Db 666 NGAYCCNGTNTTYGGNAAYCARATHATHCCNGAYACNACNATHYTNITGYCNGTNCNTT 725  
QY 745 ccatacgcccttggaaatgttactacattatcttactttagttaggacttaagttgt 804  
Db 726 YCAVCAVGCNTTYGGNACNTTYACNAAYTYNGNTAYTYTNATHHTGYGNTTYCAYGTNGT 785  
QY 805 aatgttgaagaatttgaaggcgcaacttctctaaacacatacagaattacaataccc 864  
Db 786 NYTNATGTAYMGNTTYAAYGARCAVYTNNTTYTNCARACNYTNCARGAYTAYAARTGYCA 845  
QY 865 cactatgtagtgccccctccagttatgltgttttggctaaaagcccatagtcogatca 924  
Db 846 RTCNGCNNTYNTNGTNCNACNGTNYTNGCNTTYTNGCNAAARAAYCCNYTNGNGAYAA 905  
QY 925 atagatttatacgagcttlaacggaagtgtcactgagagagctcctttagaanaagatgt 984  
Db 906 RTAYGAYYTNCAAYYTNCAVGARATHGCNTCNGGNGCNCNTNTNCNARGARAT 965  
QY 985 cgcagaagcagtagcaagaaggttgaattacctggaatcatacaagaatatgattaac 1044  
Db 966 HTCNGARATHGCNGCNAAARMGNTTYAARYTNCNGNGNATHMGNCARGGNTAYGNYTNAC 1025  
QY 1045 tgaacttgctgcgtgttaattgataccctcataatgctgtgaaaacaggttcaactg 1104  
Db 1026 NGARACNACNTGYGCNATHHTGNATHACNGCNGARGGNGARTTYAARYTNGCNGTNGG 1085  
QY 1105 aagaccttgccatatacatlaaagctaaagttttagataacgcgtactggaagcgctag 1164  
Db 1086 NAARGTNGTNCNTTYTAYTCNTNAARGTNTNGAYYTNAAYACNGGNAARAARYTNGG 1145  
QY 1165 accaggaagaagcggaatatgcttccaagtgaatgaltatgaagatatataca 1224  
Db 1146 NCCNAAYGARMGNGNGARARHTGYTTYAARGGNCNATGATHATGAARGGNTAYATHAA 1205  
QY 1225 caatccggaagcaactatgtatactattgacaaagatggttgcttcatctgagatat 1284

Query Match	32.9%	Score 580.6	DB 3	Length 1922
Best Local Similarity	59.9%	Pred. No. 3.8e-110		

	Matches	1011;	Conservative	0;	Mismatches	669;	Indels	9;	Gaps	2;
QY	16	aggatcaaat	tgagaagaaacat	taggcatt	gagagcgtcct	cgtagatagtc	ca	75		
Db	2	AAGATGGA	AGATGATAGTAA	ACATATTTAT	GCATGGCC	ACCCCATTTCTAT	CTTTGGGA	61		
QY	76	tcctgctc	gcgcagagacaaca	attatacca	atctgtataa	attgcac	cttctc	135		
Db	62	GGATGGA	ACTGCCGAGACA	CAATTC	CAACAAAGCGAT	GATGAGAGGTAT	GCACAGGTTCCAGG	121		
QY	136	agcaata	-----at	cgatgct	atacaaat	gaaagtaata	atcatatgctc	aaatattga	189	
Db	122	GACAA	TTGCTTTTAC	TGATGAC	CACACG	CAGAGGTA	AAATATACATAT	TTCCGAATATTTTGA	181	
QY	190	aaccagct	gcgccttagc	gtgtat	gatagaaca	atagctg	ctgaa	tgaaacaatgtgt	249	
Db	182	AATG	CTTGCCGAT	TAGCCGA	AACTATGA	AGAGGTAC	GGACTTGGTTT	TACAACACCACAT	241	
QY	250	gggtgat	gcagtgaaaaca	tataaact	ttttta	atcctgt	cctgtc	gtcgttatact	309	
Db	242	TGCTG	TTGTAGTGA	AACTTCT	CTCAGT	TTTTTAT	GGCTGTATG	CGGTGACCTATTTAT	301	
QY	310	aggaata	ccagtagcaaca	tcaaat	gatata	gtacacaga	tygagag	ttaactgtcat	369	
Db	302	TGGG	TTGGAGTTGC	ACCACA	CAATGATAT	TTACAATGA	CGTGAATTTAT	TACAACAGTTT	361	
QY	370	gaatata	ccaaccca	atcatgt	tttag	ttcaaga	aagcact	cccgtlat	429	
Db	362	GTTCA	TATCACAC	CTACATA	GTATTTT	GTCTAA	AAGAGCGCT	CCAAAAAATCCTAGG	421	
QY	430	agta	cagcaaat	ctaag	tttcat	ttaaaaa	agtcgt	agttat	489	
Db	422	GGTACA	AAAGAAAT	TACCTGT	ATTCAG	AAAAAT	GTATTTCTG	GATTTCTCGAGAGGATTA	481	
QY	490	taat	gcgltgaat	gcgtat	ctac	cttgt	gtcag	gttata	549	
Db	482	TATGG	GAACAATCT	ATGTACT	CGTTCA	TGGAATCT	CAATTTAC	CTGCAGGTTTAAATGA	541	
QY	550	atgt	catttac	accacaa	aagatt	ttgat	c	cccttg	609	
Db	542	ATATG	ATTACATAC	CGGATTTCT	TTTGAC	CGGAAAC	GACGACG	CACTTATATGAATTC	601	
QY	610	atct	gaca	actg	atgtgc	ctaag	gtgt	agtag	669	
Db	602	ATCGG	ATCTACTG	GAATTA	CCCAAG	AGGTGAT	CTTACT	CAATGAATGTTGTGTAG	661	
QY	670	atc	gtlcat	agcagga	tcccat	ttat	gycact	cgtag	729	
Db	662	ATTTT	CTCACTG	CAGAGAT	CCGTGT	TTGGTA	ATCAAAAT	ATTTCCGATAC	721	
QY	730	ttc	cttag	tacc	gttcc	atg	ccttg	aatgt	789	
Db	722	AACAG	TTATACCAT	TTTCAT	GTGTTT	CCAAATG	TTTACA	CAATTAGATAC	781	
QY	790	agga	ctta	aggtgt	gtaagt	ttga	agaaat	ttgag	849	
Db	782	TGGAT	TTTCGTAT	TGTGCTT	ATGTAT	AGATTTGA	AGAGGAAT	TATTTTACGAT	841	
QY	850	gaat	tacaaa	atcccc	actat	gttag	tggcc	ctccag	909	
Db	842	AGAT	TATAAAT	TCAAGT	TGCGTT	GCTGTG	TACCTTAC	CCCTATTTTCA	901	
QY	910	cccat	tagt	cgat	caat	atga	ttat	c	969	
Db	902	CACAT	TAGTGC	GAACAAT	TACGAT	TTTAT	TCCAACTT	TACATGA	961	
QY	970	ttta	gaaa	agat	gtcgc	agaag	cagtag	caaga	1029	
Db	962	TCTCG	GAAGAAG	ATTGGA	GAGCGGT	AGCAAA	ACGTTTTA	AGTTGCCGGCAT	1021	
QY	1030	agga	tatga	ttaact	gaaact	gtcgt	cgctg	taatga	1089	
Db	1022	AGGGT	ACGACTT	ACGAACT	ACTAC	CTATAT	TATTA	TACACCGAAGGGGAT	1081	

QY	1090	aacaggttcaactggaagacccttgcacatataaagctaagtttagataacgctac	1149
Db	1082	ACCGGAGCATGTGGTAAGTCGTTCCATTCTTACGGCCAAATGTGTGATCTGGATAC	1141
QY	1150	tggaagcgctagagaccaggaagagcgcaaatatgctttcaagtgaatgattat	1209
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DEFINITION	INLUCPROT		
ACCESSION	L.noctiluca mRNA for luciferase protein.		
VERSION	X89479		
KEYWORDS	X89479.1 GI:899314		
SOURCE	luciferase.		
ORGANISM	Lampyris noctiluca.		
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AUTHORS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
TITLE	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;		
JOURNAL	Elateriformia; Cantharoidae; Lampyridae; Lampyris.		
MEDLINE	1 (bases 1 to 1725)		
REFERENCE	Sala-Newby, G.B., Thomson, C.M. and Campbell, A.K.		
AUTHORS	Sequence and biochemical similarities between the luciferases of		
TITLE	the glow-worm Lampyris noctiluca and the firefly Photinus pyralis		
JOURNAL	Biochem. J. 313 (Pt 3), 761-767 (1996)		
FEATURES	96190714		
source	2 (bases 1 to 1725)		
	Sala-newby, G.B.		
	Direct Submission		
	Submitted (07-JUL-1995) G.B. Sala-Newby, University of Wales		
	College of Medicine, Department of medical biochemistry, Heath		
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Best Local Similarity 60.0%; Pred. No. 4.2e-110;
Matches 1006; Conservative 0; Mismatches 661; Indels 9; Gaps 2;

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DEFINITION	photuris pennsylvanica luciferase mRNA, complete cds.				

ACCESSION	U31240
VERSION	U31240.1
KEYWORDS	GI:2190534 Firefly luciferase. Photuris pennsylvanica.
SOURCE	Photuris pennsylvanica
ORGANISM	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidea; Lampyridae; Photuris.
REFERENCE	1 (bases 1 to 1831) Ye, L., Buck, L.M., Schaeffer, H.J. and Leach, F.R. Cloning and sequencing of a cDNA for firefly luciferase from Photuris pennsylvanica
AUTHORS	Biochim. Biophys. Acta 1339 (1), 39-52 (1997)
TITLE	97307756
JOURNAL	Dr. Keith Wood of Promega Corporation has cloned two cDNAs for Photuris pennsylvanica from fireflies collected in Maryland. One of the corresponding protein sequences differs by only two amino acids from that reported herein.
MEDLINE	2 (bases 1 to 1831) Leach, F.R.
REMARK	Direct Submission Submitted (07-JUL-1995) Biochemistry & Molecular Biology, Oklahoma State University, 246 B Noble Research Center, Stillwater, OK 74078-3035, USA
REFERENCE	On Jun 11, 1997 this sequence version replaced gi:927311.
AUTHORS	Location/Qualifiers
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[illegible]



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DEFINITION AX074308  
ACCESSION AX074308  
VERSION AX074308.1 GI:12710494  
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AUTHORS  
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RESULT 11

AX074303

LOCUS

DEFINITION Sequence 17 from Patent WO0104310.

ACCESSION AX074303

VERSION AX074303.1 GI:12710489

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

synthetic construct.  
artificial construct  
1 (bases 1 to 2268)  
Weber,E.R., Wood,K.V. and Hall,M.P.  
Fc epsilon receptor-luminescence inducing protein chimeric nucleic acid molecules, fusion proteins and uses thereof  
Patent: WO 0104310-A 17 18-JAN-2001;  
Heska Corporation (US) ; PROMEGA CORPORATION (US)  
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VERSION		AX074300.1 GI:12710486	
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AUTHORS		Weber,E.R., Wood,K.V. and Hall,M.P.	
TITLE		Fc epsilon receptor-luminescence inducing protein chimERIC nucleic	
JOURNAL		acid molecules, fusion proteins and uses thereof	
		Patent: WO 0104310-A 14 18-JAN-2001;	
		Heska Corporation (US) ; PROMEGA CORPORATION (US)	
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ACCESSION AX074302  
VERSION AX074302.1 GI:12710488  
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
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REFERENCE  
AUTHORS 1 (bases 1 to 1638)  
Weber, E.R., Wood, R.V. and Hall, M.P.  
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic

acid molecules, fusion proteins and uses thereof  
Patent: WO 0104310-A 16 18-JAN-2001;

Heska Corporation (US) ; PROMEGA CORPORATION (US)

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source location/Qualifiers

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Best Local Similarity 60.0%; Pred. No. 9.8e-109;

Matches 978; Conservative 0; Mismatches 647; Indels 6; Gaps 1;

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QY 920 gatcaatagattatcgaactgaagagtgctactgagagagctcccttagga 979

Db 738 GAAAGTACGATTTATCGCACTTAAAGAAATTTGCATCTGTTGGCGCACCTTTATCAAAA 679

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QY 1100 actggaagacccttgccatataaagctaaagttttagataaacgctactgggaagcg 1159

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Db 18 CACAAATCTAA 8

RESULT 15

AX098293

LOCUS

DEFINITION

AX098293

AX098293

AX098293.1

GI:13537597

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Sequence 12 from Patent WO0120002.  
1 (bases 1 to 1642)  
Wood, K.V., Hall, M.P. and Gruber, M.  
Thermotaxable luciferases from Photuris pennsylvanica and pyrophorus  
plagiophthalmus and methods of production  
Patent: WO 0120002-A 12 22-MAR-2001;  
PROMEGA CORPORATION (US)  
Location/Qualifiers  
1. .1642

FEATURES

source

/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="mutant luciferase"  
BASE COUNT 559 a 255 c 322 g 506 t  
ORIGIN

Query Match 32.4%; Score 571.6; DB 6; Length 1642;  
Best Local Similarity 59.9%; Pred. No. 2.8e-108;  
Matches 977; Conservative 0; Mismatches 649; Indels 6; Gaps 1;

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QY 85 ggcaggaacaacaatlataccaatcattgtaataattgcattcttcctg-----aagc 138  
DB 67 GGCTGGAGAACAGATGTTTACGCATTATCTCGTTATGCAGATATTTTCAGGATGCATTAGC 126  
QY 139 aataatcgatgctcatacaataatgaagtaatatcatatgctcaaatattgaaaccagctg 198  
DB 127 ATTGACAAATGCTCATACAAAGAAATGTTTATATGAAGAGTTTAAAAATGTGCGTG 186  
QY 199 ccgcttagctgttagatagaacaatatgcttgtaatgaanaacaatgttggtggtatg 258  
DB 187 TCGTTTAGCGGAAGTTTAAAAAGTATGGATTAAAACAAACGACACAAATAGCGGTGTG 246  
QY 259 cagtgaaacaacataataaactttttaaactcgtccctgctgcttataacttaagaaatacc 318  
DB 247 TAGCGAAAAATGGTTTGCATTTTCTCCTTAAATTGCATCATTTGTATCTTGGAAATAAT 306  
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QY 499 tgaatgcgtatctacacttctgttcgacgttatactgacacacacttctgattcattgcatc 558  
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DB 847 AGTGAAAGTACTTTACTTGTACCAACATTAATGGCATTTTTCAAAAAGTGCATTAGT 906  
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QY 1039 attaactaaaacttgcgtgcgtgtaatgattacccctcataatgctgtgtaaaaacaggttc 1098  
DB 1027 ATTAACAGAAACCACTTCGGCTGTTTAAATTATACACCGGACACTGACGTCAGACCGGGATC 1086  
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DB 1087 AACTGGTAAATAGTACCATTTCACGCTGTTAAAGTTGTCGATCCTACAAACAGGAAAAAT 1146  
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DB 1147 TTTGGGGCCAAATGAACCTGGAGATTGTATTTTAAAGCGACATGATTAATGAAGTTA 1206  
QY 1219 ttacaacaatccggaagcaactatgtatactatgtgacaagaatggttgcttcaattcgtg 1278  
DB 1207 TTATAATATGAAGAAGCTACTTAAGCAATTATTAAACAAAGACGGATGTTGCGCTCTGG 1266  
QY 1279 agatatgatatatacagacgaagatgaaatltccttataagttgatacgaatlaaagaact 1338  
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DB 1327 AATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAATTTGAGGGAATACTCTTACAAACA 1386  
QY 1399 tccaagtaattgctgatgcggtgttactgagttccggaacaaatttgttgacaattacc 1458  
DB 1387 TCCGTAATTTGTTGATGCCGGCGTTACTGTATACCGGATGAAGCCGGCGGAGCTTCC 1446  
QY 1459 tgcgtcgtgtgtgtgttagaatttgcgaagacgctgtaactgaaagaagtttcaagattt 1518  
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QY 1639 gcgagcaccaaa 1650  
DB 1627 ACACAAATCTAA 1638

Search completed: September 7, 2002, 22:27:04  
Job time: 9238 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 15:03:41 ; Search time 30.72 Seconds  
(without alignments)  
3069.083 Million cell updates/sec

Title: US-09-993-874-2  
Perfect score: 2812  
Sequence: 1 MEEENIRGERPRDIVHPSG.....KLIRKELREIFAQRAPKSKL 545

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_prodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvivirus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2812	100.0	545	5 Q9U4U8	Q9U4U8 phrixothrix
2	2099.5	74.7	546	5 Q9U4U7	Q9U4U7 phrixothrix
3	1583.5	56.3	550	5 Q27755	Q27755 photinus py
4	1557.5	55.4	550	5 Q27758	Q27758 photinus py
5	1534	54.6	547	5 Q27688	Q27688 lampyris no
6	1519	54.0	552	5 Q94696	Q94696 photuris pe
7	1515	53.9	552	5 Q94697	Q94697 photuris pe
8	1511.5	53.8	548	5 Q26076	Q26076 pyrocoelia
9	1510.5	53.7	548	5 Q9GPF9	Q9GPF9 pyrocoelia
10	1485	52.8	548	5 Q25118	Q25118 hotaria par
11	1483	52.7	548	5 Q26304	Q26304 luciola min
12	1457.5	51.8	548	5 Q27348	Q27348 luciola lat
13	1454	51.7	545	5 Q27757	Q27757 photuris pe
14	1453.5	51.7	548	5 Q27321	Q27321 luciola lat
15	1030	36.6	544	5 Q9VCC6	Q9VCC6 drosophila
16	864.5	30.7	542	10 Q42943	Q42943 nicotiana t

17	847.5	30.1	636	10 Q42879	Q42879 lithospermum
18	847	30.1	548	10 Q48868	Q48868 populus bal
19	834	29.7	545	10 Q9SWH8	Q9SWH8 solanum tub
20	828	29.4	562	10 Q9FGW4	Q9FGW4 arabidopsis
21	826.5	29.4	540	10 Q94G19	Q94G19 populus bal
22	824.5	29.3	544	10 Q94L50	Q94L50 rubus idaeu
23	823.5	29.3	557	10 Q48869	Q48869 populus bal
24	820.5	29.2	544	10 Q9M0X9	Q9M0X9 arabidopsis
25	817.5	29.1	536	10 Q941M4	Q941M4 populus tom
26	816.5	29.0	536	10 Q941M3	Q941M3 populus tom
27	815.5	29.0	535	10 Q81139	Q81139 populus tre
28	810	28.8	546	10 Q9C5H2	Q9C5H2 arabidopsis
29	802	28.5	585	10 Q42880	Q42880 lithospermum
30	800	28.4	542	10 Q9FOY7	Q9FOY7 capsicum an
31	795	28.3	570	10 Q9LU36	Q9LU36 arabidopsis
32	790.5	28.1	556	10 Q9MW52	Q9MW52 lolium pere
33	783	27.8	580	10 Q9LMV8	Q9LMV8 arabidopsis
34	780	27.7	544	5 Q19339	Q19339 caenorhabdit
35	777.5	27.6	570	10 Q81140	Q81140 populus tre
36	777	27.6	579	10 Q94G18	Q94G18 populus bal
37	777	27.6	1549	10 Q9LMV7	Q9LMV7 arabidopsis
38	776	27.6	522	2 Q9K3W1	Q9K3W1 streptomyces
39	768.5	27.3	557	10 Q9M7S1	Q9M7S1 lolium pere
40	767.5	27.3	543	10 Q9L449	Q9L449 rubus idaeu
41	752.5	26.8	566	10 Q49414	Q49414 arabidopsis
42	746.5	26.5	542	10 Q9LQ12	Q9LQ12 arabidopsis
43	732	26.0	597	5 Q9Y158	Q9Y158 drosophila
44	719.5	25.6	570	10 Q9M7S3	Q9M7S3 lolium pere
45	708.5	25.2	591	10 Q9L451	Q9L451 rubus idaeu

ALIGNMENTS

RESULT	ID	Q9U4U8	PRELIMINARY:	PRT:	545 AA.
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DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE	LUCIFERASE.				
OS	Phrixothrix vivianli.				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;				
OC	Elateriformia; Cantharidae; Phengodidae; Phrixothrix.				
OX	NCBI_TaxID=94780;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-99315203; PubMed-10387072;				
RA	Vivianli V.R., Bechara E.J., Ohmura Y.;				
RT	"Cloning, sequence analysis, and expression of active Phrixothrix				
RT	railroad-worms luciferases: relationship between bioluminescence				
RT	spectra and primary structures."				
RL	Biochemistry 38:8271-8279(1999).				
DR	EMBL; AF139644; AAD34542.1; -				
DR	HSSP; P08659; LICI.				
DR	InterPro; IPR000873; AMP-bind.				
DR	Pfam; PF00501; AMP-binding; 1.				
DR	PROSITE; PS00455; AMP_BINDING; 1.				
SQ	SEQUENCE 545 AA; 59756 MW; 3C7971D40E4BC119 CRC64;				
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QY	Best local Similarity	100.0%;	Pred. No. 6.5e-209;		
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Db 61 AVSIEQYGLNENNVCSENNINFNPVLAALYLGI PVATSNDMYTDGELTGHNLISKP 120  
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Db 121 TIMSSSKALPLILRVQONLSFIKKVVVIDSMYDINGVECVSTFVARYTDHTFDPLSFTP 180  
QY 181 KDFDPLEKIALIMSSSGTTGLPKGVVLSHRSLTIRFVHSRDPITYGTRVPQTSILSLVPE 240  
Db 181 KDFDPLEKIALIMSSSGTTGLPKGVVLSHRSLTIRFVHSRDPITYGTRVPQTSILSLVPE 240  
QY 241 HHAFGMFTLSYFVVGKLVVMLKKFEGALLFKTIQNYKIPTIIVAPVPMVFLAKSPLVDQ 300  
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Db 361 RPLPYIRAKVLDNATGKALGPGEIGEICFQSEMIKGYNNPEATIDTIDKDGWLHSGDI 420  
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Db 421 GYYDEDEGNFIVDLRLKELIKKYGYQVAPAELENLLQHPISADAGVTGPVDEFGQLPAA 480  
QY 481 CVLLESGKLTLEKEVODFIAAQVTPTKHLRGVVFVDSIPKPTGKLIRKELREIFAQRA 540  
Db 481 CVLLESGKLTLEKEVODFIAAQVTPTKHLRGVVFVDSIPKPTGKLIRKELREIFAQRA 540  
QY 541 PKSKL 545  
Db 541 PKSKL 545

RESULT 2  
Q9U4U7  
ID Q9U4U7 PRELIMINARY; PRT; 546 AA.  
AC Q9U4U7;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE RED-BIOLUMINESCENCE ELICITING LUCIFERASE.  
OS Phrixothrix hirtus.  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
OC Elateriformia; Cantharoidea; Phengodidae; Phrixothrix.  
OX NCBI\_TaxID=94779;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99315203; PubMed=10387072;  
RA Viviani V.R., Bechara E.J., Ohmiya Y.;  
RT "Cloning, sequence analysis, and expression of active Phrixothrix  
RT railroad-worms luciferases; relationship between bioluminescence  
RT spectra and primary structures.";  
RL Biochemistry 38:8271-8279(1999).  
DR EMBL; AF139645; AAD34543.1; -.  
DR HSSP; P08659; 1LCI.  
DR InterPro; IPR000873; AMP-bind.  
DR Pfam; PF00501; AMP-binding; 1.  
DR PROSITE; PS00455; AMP\_BINDING; 1.  
SQ SEQUENCE 546 AA; 60952 MW; 9349ABC931CC9A50 CRC64;

Query Match 74.7%; Score 2099.5; DB 5; Length 546;  
Best Local Similarity 71.1%; Pred. No. 7.8e-154;  
Matches 391; Conservative 84; Mismatches 66; Indels 9; Gaps 3;

QY 1 MEEENIRHGERPRDIVHPGSAGQOLYQSLYKFASFPEALIDAHTNEVISAQIFETSCRL 60  
Db 1 MEEENYVNGDRPRDLVFPGTAGLQLYQSLYKYSYITDGIIDAHTNEVISAQIFETSCRL 60  
QY 61 AVSIEQYGLNENNVCSENNINFNPVLAALYLGI PVATSNDMYTDGELTGHNLISKP 120

Db 61 AVSLEKYGLDHNNVVAICSENNIHFFGPPLIALLYQGI PMATSNDMYTEREMIGHNLISKP 120  
QY 121 TIMSSSKALPLILRVQONLSFIKKVVVIDSMYDINGVECVSTFVARYTDHTFDPLSFTP 180  
Db 121 CLMFCSKSLPFLIKQKHLDFELKRVIVIDSMYDINGVECVSFSDSRNTDHAFDVKKFNP 180  
QY 181 KDFDPLEKIALIMSSSGTTGLPKGVVLSHRSLTIRFVHSRDPITYGTRVPQTSILSLVPE 240  
Db 181 KEFDPLERTALIMTSSSGTTGLPKGVVISHRSITIRFVHSSDPITYGTRIAPDSTIIAIAPE 240  
QY 241 HHAFGMFTLSYFVVGKLVVMLKKFEGALLFKTIQNYKIPTIIVAPVPMVFLAKSPLVDQ 300  
Db 241 HHAFLFTALAYFPVGLKIVVKKFEGEFLLKTIQNYKIASIVPPIMVYLAKSPLVDE 300  
QY 301 YDLSLITEVATGAPLPGKDVAAEAVAKRLKLPGIIOGYGLTETCCAVMITPHN-AVKTGST 359  
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QY 360 GRPLPYIRAKVLDNATGKALGPGEIGEICFQSEMIKGYNNPEATIDTIDKDGWLHSGD 419  
Db 361 GTPMPYQVQVIDINTGKALGPKEIGEICFKSQMLMKGYHNNPQATRDALDKDGLHTGD 420  
QY 420 IGYDEDEGNFIVDLRLKELIKKYGYQVAPAELENLLQHPNISADAGVTGPVDEFGQL-- 477  
Db 421 LGYYDEDRFIYVVDRLKELIKKYGYQVAPAELENLLQHPNISDAGVI---EFTNLV 476  
QY 478 --PAACVYLESGKLTLEKEVODFIAAQVTPTKHLRGVVFVDSIPKPTGKLIRKELREI 535  
Db 477 NYLSACVYLEPGKTMTEKEVQDYIAELVTTTKHLRGVVFVDSIPKPTGKLIRNELRAI 536  
QY 536 FAQAPRPSKL 545  
Db 537 FAREQAKSKL 546

RESULT 3  
Q27755  
ID Q27755 PRELIMINARY; PRT; 550 AA.  
AC Q27755;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE FIREFLY LUCIFERASE (EC 1.13.12.7).  
GN LUC.  
OS Photinus pyralis (North American firefly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
OC Elateriformia; Cantharoidea; Lampyridae; Photinus.  
OX NCBI\_TaxID=7054;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Croizier G.;  
RT "Construction and utilization of an Autographa californica nuclear  
RT polyhedrosis virus vector with a unique cloning site: expression of  
RT genes amplified by the polymerase chain reaction.";  
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X84846; CAA59281.1; -.  
DR HSSP; P08659; 1BA3.  
DR InterPro; IPR000873; AMP-bind.  
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DR PROSITE; PS00455; AMP\_BINDING; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 550 AA; 60731 MW; 0A1CC749D0C96ADD CRC64;

Query Match 56.3%; Score 1583.5; DB 5; Length 550;  
Best Local Similarity 55.5%; Pred. No. 6.1e-114;  
Matches 305; Conservative 102; Mismatches 138; Indels 5; Gaps 3;

QY 1 MEE-ENIRHGERPRDIVHPGSAGQOLYQSLYKFASFPE--AIDAHTNEVISAQIFETS 57  
Db 1 MEDAKNIKKGPAFPYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVNTIYAEYFEMS 60





Query Match	53.98;	Score 1515;	DB 5;	Length 552;
Best Local Similarity	52.48;	Pred. No. 1.2e-108;		
Matches 285;	Conservative 104;	Mismatches 151;	Indels 4;	Gaps 3;

QY 3 EENIRHGERPRDVLVHPGSAGOOQLYSOLYKFASPE--AIIDAHTNEVISYAQIFETSCRL 60  
| | | | :  
Db 4 ENNILIGPPPIYPTEEGTAGEOQLHRAISRIFAAPGTLAYTDVHTELEVITYKEFLDYTCRL 63

QY 61 AVSIEOYGLNENNVAVCSENNINFENPVLAALYLGI PVATSDMYTDDGELTGHNLISKP 120  
| :  
Db 64 AEAMKNYGLGLOHTISVCSENCVOEFMPICALYGVATAPTNDIYNRELXSLISIQP 123

QY 121 TIMFSSKKALPLLRVQONLSFIKKVVVIDSMYDINGVECVSTFVARYTDTHEPDLSTFP 180  
| :  
Db 124 TVVFTSRNSLQKILGVQSRLPIIKKIILLDGKDYLGYSQMOSFMKEHVPAFNVSFAFKP 183

QY 181 KDEFDPLEKIALIMSSGGTGLPKGVNLSHRSLTRFVHSRPDIYGTRTPQTSLIVPE 240  
| | :  
Db 184 LSF-D-LDRVACIMSSSGSTGLPKGPISHRNITRFSHCRDPVEGNQIIPOTTILCAVPF 242

QY 241 HHAFGMETTLYFEVGLKVMLKKFEGALFLKTIONYKIPTIVARPVMVELAKSPLYDQ 300  
| | | | | | | | | | :  
Db 243 HHAFGTFTNLGYLICGFHVLMYRFNEHLFLTODYKCQSAALLVPTVALAFLAKNPLOYDK 302

QY 301 YDLSLTLEVATGCARGLKDVAAEAVAKRLKPGITOGYGLTETCCAVMITPHNAVKTGSTG 360  
| | | | :  
Db 303 YDLSNLHEIASGCAPLSKSEISAIAKRKFLPGIROGYGLTETTCAIVITAEGEFKLGAVG 362

QY 361 RPLPYIKAKVLDMATGKALGPGERGEICFOSEMIMKGYYNPPEATIDTIDKDGWLHSGDI 420  
: : : : | | | | | | | | | | :  
Db 363 KVPPEYSLKVLDMNTGKKLGPNERGEICFKGPMIMKGYINNPPEATRELIDEEGWHSGLDI 422

QY 421 GYDEDGNFFIVDRLELIKYYKYOVAPAELLENLLQHPSIADAGVTGVPDEFQGOLPAA 480  
| : : : : : : : : : : | | | | | | | | | | | | | | | | | | | | | |  
Db 423 GFDEDEGHVIYDRLSKSLIKYKGYOVPPAELEALLQHPIEDAGVAGVPDEVAGDLPGA 482

QY 481 CVVLESCKTLTEKEVODFIAAQVTPTKHLRGVNVDSIPKGPCTGLIRKELREIFAQRA 540  
| | :  
Db 483 VVVLKEGKSITEKEIQDYVAGQVTSKKLRGVEFVKVPKGTGKIDTRKIKEILI-KA 541

QY 541 PKSK 544  
| |  
Db 542 QKKG 545

RESULT 8  
ID Q26076 PRELIMINARY; PRT; 548 AA.  
AC Q26076;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE LUCIFERASE.  
OS Pyrocoelia miyako.  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;  
OC Elateriformia; Cantharoidea; Lampyridae; Pyrocoelia.  
OX NCBI\_TaxID=39363;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96061635; PubMed=7480137;  
RA Ohmura Y., Ohba N., Toh H., Tsuji F.;  
RT "Cloning, expression and sequence analysis of cDNA for the luciferases  
from the Japanese fireflies, Pyrocoelia miyako and Hotaria parvula.";  
RL Photochem. Photobiol. 62:309-313(1995).  
DR EMBL: L39928; AAC37254.1; -.  
DR HSSP: P08659; ILCT.  
DR InterPro: IPR000873; AMP-bind.  
DR InterPro: IPR000215; Serpin.  
DR Pfam: PF00501; AMP-binding; 1.  
DR PROSITE: PS00455; AMP\_BINDING; 1.

DR PROSITE; PS00284; SERPIN; UNKNOWN\_1.  
SQ SEQUENCE 548 AA; 60956 MW; CD37F63E982A9401 CRC64;

Query Match	53.8%;	Score 1511.5;	DB 5;	Length 548;
Best Local Similarity	52.9%;	Pred. No. 2.2e-108;		
Matches 289;	Conservative 103;	Mismatches 151;	Indels 3;	Gaps 2;

QY	2	EEENIRHGERRDVIHPGSAGQOLYOSLYKFASFPE--AIDTAHNEVISYAQIFENSCR	59
		: : :       : :   :   :   : : : :       :   :   :	
Db	4	DSKIHMHGHRHSILMEDGTAGEQLHKAMKRYAQPPTIAFTDAHAENVITYSEYFEMSCR	63
QY	60	LAVSIEQYGLNENNVGVCSENNINFPVLAALYLGIPAVATSNMYTDELTHGNISK	119
		: : :       : :       : :       : :     :     :	
Db	64	LAETMKRYGLQHHIAVCSETSLQFEMFVCGALFIGVGAAPTNDIYNERELYNLSFIQ	123
QY	120	PTIMSSSKALPLLRVQONLSFIKKVVVIDSMYDINGVEGVSTFVARYTDTHTFDPLSFT	179
		:   :   :       :   :   :   :     : : : :   : : : :	
Db	124	PTIVECSKRALQKILGVQKKLPVIOKILVDSREDYMGQKMSFIESHLPAGFNEYDYI	183
QY	180	PKDFDPLEKIALIMSSSGTGLPKGVVLSHRSLTIRFVHSRDPITYGTRVPQTSILVP	239
		:   :   :   :   :   :   :   :   :   :   :   :   :	
Db	184	PDSFDRETATALIMNSSGSTGLPKGVDLTHMNVCVRFSHCRDPVFGNOIIPDTALITVIP	243
QY	240	FHHAFGMFTTLSYFVVGKLVMLKKFEGALFKTIONYKPIPIVAPVPMVELAKSPLVD	299
		: : : : :   : : : : :   : : : :	
Db	244	FHHVFQMTTGLYLCGFRIVLMYRFEELEFLRSLQDYKIQSALLVPTLFSFAKSTPLVD	303
QY	300	QYDLSLLEVATGGAPLGKDVAEAVAKRULKPGIIQGYGLTEPCCAVMITPHNAVYKTSST	359
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	304	KYDLSNLHETIASGAPLAKAVEGAIVAKREKLPGRQGYGLTETSALITTEPGDKRGAC	363
QY	360	GRPLPYIKAKVLNATGKALGPERGECICFOSEMIKGYVNNDEATIDTIDKDGWLHSGD	419
		: : :   :   :   :       :   :   :   :   :   :   :   :   :	
Db	364	GKVVPFTAKIYDLDTGKTGLGVNORGEIJCVPIMIMKGYVNNDEATINALIDKDGWLHSGD	423
QY	420	IGYDDEDEGNFIYDRKLKELIKYGYQVAPAELENLLQHPSTADAGVTGVPDEFGGOLPA	479
		:   :   :   :   :       :   :   :   :   :   :   :   :	
Db	424	IAYYDKDGHFIIYDRKLSLIKYGQVPAELESILLQHPFIFDAGVAGIPDPDAGELPA	483
QY	480	ACVVLSESKTLTEKEVQDEFTIAAQVTPTKHLRGVVFVDSIPKGPCTGLIRKELREIFAQR	539
		:   :   :   :   :   :   :   :   :   :   :   :	
Db	484	AVVLEEGKMMEQEVMDYVAGQVTAASKRLRGVKFVDEVPKGLTKIDSRKIREILTM-	542
QY	540	APKSKL 545	
Db	543	GOKSKL 548	

RESULT	9		
ID	Q9GPF9	PRELIMINARY;	PRT; 548 AA.
AC	Q9GPF9;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	LUCIFERASE.		
OS	Pyrocoelia rufa.		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;		
OC	Elateryiformia; Cantharoidae; Lampyridae; Pyrocoelia.		
OX	NCBI_TaxID=71223;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LIGHT ORGAN;		
RA	Lee K.S., Park H.J., Bae J.S., Lee K.S., Shon H.D., Jin B.R.;		
RT	"Molecular Cloning and Expression of cDNA encoding luciferase from the		
RT	firefly, Pyrocoelia rufa.";		
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF328553; AAG45439.1; -.		
DR	HSSP; P08659; 1LCI.		
DR	InterPro; IPR000215; Serpin.		
DR	PROSITE; PS00284; SERPIN; UNKNOWN_1.		



SQ SEQUENCE 548 AA; 60787 MW; FE86DEB7DDDFEA9B CRC64;

Query Match	53.7%;	Score 1510.5;	DB 5;	Length 548;
Best Local Similarity	52.9%;	Pred. No. 2.7e-108;		
Matches 289;	Conservative 103;	Mismatches 151;	Indels 3;	Gaps 2;

QY	2	EEENIRHGERRDIVHPGSAGQOLYSLYKFASFPE--AIIDAHTNEVISYAQIFETSCR	59
Db	4	DSKIHMHGHRHSILMEDGTAGEOLHKAMKRYAQAOPGTIAFTDAHAENVITYSEYFEMSCR	63
QY	60	LAVSIEQYGINENNVCSENNINEFNPVLAALYLGPVATSNDMYTDELTGHLNTSK	119
Db	64	LAETMKRYGLQHHIAVCSENSLQFEMPVCALFIGVGAFTNDIYNERELYNLSLFSIQ	123
QY	120	PTIMFSSKKALPLILRVQONLSFIKKVVIDSMYDINGVECVSTFVARYTDHTFDPLST	179
Db	124	PTIVECSKRALQKILGVHKKLPVIOKIVILDSREDYMGKQMSYFIESHLPAGFNEYDI	183
QY	180	PKDFDPLEKALIMSSSGTGLPKGVLSHRSLTIRFVHSRDPYIGTRTPQTSILSV	239
Db	184	PDFDRETATALIMSSSGTGLPKGVLDTHMNCVRFSHCRDPVFGNOIIPDTAILTV	243
QY	240	FHHAFGMEFTLLSYFVVGKLVMLKKREGALFELKTIONYKPIPTIVAPVMVFLAKSPVD	299
Db	244	FHHGFGMEFTLLGYLTCGFRIVLWRFEEELFLRSLQDYKKISALLVPTLFSFAKSTLVD	303
QY	300	QYDLSLFEVATGAPLKGDAEAVAKRLKLPGIIOGYGLTETCCAVMITPHNAVKTGST	359
Db	304	KYDLSNLHEIASGGAPLAKVEGEAVAKRFLPGIRQGDGLTETTSALIIITPEGDKKGAC	363
QY	360	GRPLPYIAKAVLDNATGKALGPGEGEICFQSEMIKGYVNPPEATIDTIDKDGWLHSGD	419
Db	364	GKVPPEFAKIVLDLDTGKTLGVNQGELCVKGPIMKGYVNPPEATNALIDKDGWLHSGD	423
QY	420	IGYYDEDDGNFEIVDLKELIKYKGVOVAPAELENLLQHPSTADAGVTGVPDEFGGQJPA	479
Db	424	IAYYDKDGHFIVDLKSLIKYKGVOVPALESILLQHPFIIDAGVAGIPDPDAGELPA	483
QY	480	ACVVLSESKTLLTEKEVQDFIAQVYPTKHLRGVVFVDSIPKGPCTGKLIRKELREIFAQR	539
Db	484	AVVVLIEGKMTEQEVMDYVAGVYATASKRLRGVVKFVDEVPKGLTGKIDSRKIREIILTM-	542
QY	540	APKSKL 545	
Db	543	GOKSKL 548	

RESULT	ID	PRELIMINARY;	PRT;	548 AA.
Q25118	Q25118			
AC	Q25118;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	LUCIFERASE.			
GN	LUCIFERASE.			
OS	Hotaria parvula.			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;			
OC	Elateriformia; Cantharoidae; Lampyridae; Hotaria.			
OX	NCBI_TaxID=39323;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96061635; PubMed=7480137;			
RA	Ohmiya Y., Ohba N., Toh H., Tsuji F.;			
RT	"Cloning, expression and sequence analysis of cDNA for the luciferases			
RL	from the Japanese fireflies, <i>Pyrocoelia miyako</i> and <i>Hotaria parvula</i> ."			
DR	Photochem. Photobiol. 62:309-313(1995).			
DR	EMBL; L39929; AAC37253.1; -.			
DR	HSSP; P08659; 1LCI.			
DR	InterPro; IPR000873; AMP-bind.			
DR	Pfam; PF00501; AMP-binding; 1.			

DR	PROSITE; PS00455; AMP_BINDING; UNKNOWN_1.
SQ	SEQUENCE 548 AA; 60365 MW; 9694F3EB496CAB85 CRC64;

Query Match	52.8%;	Score 1485;	DB 5;	Length 548;
Best Local Similarity	52.0%;	Pred. No. 2.5e-106;		
Matches 284;	Conservative 106;	Mismatches 152;	Indels 4;	Gaps 3;

[illegible]

RESULT	11		
Q26304			
ID	Q26304	PRELIMINARY;	PRT; 548 AA.
AC	Q26304;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)	
DE	LUCIFERASE.		
GN	LUCIFERASE.		
OS	Luciola mingrellica (Southern Russian firefly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;		
OC	Elateriformia; Cantharoidea; Lampyridae; Luciola.		
OX	NCBI_TaxID=27446;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93277944; PubMed=8504162;		
RA	Devine J.H., Kutuzova G.D., Green V.A., Ugarova N.N., Baldwin T.O.;		
RT	"Luciferase from the east European firefly <i>Luciola mingrellica</i> : cloning		
RT	and nucleotide sequence of the cDNA, overexpression in <i>Escherichia</i>		
RT	<i>coli</i> and purification of the enzyme.";		
RL	Biochim. Biophys. Acta 1173:121-132(1993).		
DR	EMBL; S61961; AAB26932.1; -.		
DR	HSSP; P08659; IICI.		

DR	InterPro; IPR000873; AMP-bind.	
DR	Pfam; PF00501; AMP-binding; 1.	
DR	PROSITE; PS00455; AMP_BINDING;	UNKNOWN_1.
SO	SEQUENCE 548 AA; 60495 MW;	62C8953BDFBFC423 CRC64;

Query Match	52.7%;	Score 1483;	DB 5;	Length 548;
Best Local Similarity	52.0%;	Pred. No. 3.6e-106;		
Matches 284;	Conservative 107;	Mismatches 151;	Indels 4;	Gaps 3;

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Oy  2 EENIRHGERPDIVHPGSAGQOLYQSLYKRA5PE-AIIDAHTNEVISAQIETSCRL 60
    :||: :| : ||||| :||: :||: :||: :||: :||:
Db  5 KEENVVYGPLPEFYIEEGSAGIQLHKYMHQYAKGAIASFNAITGVDISYQEFDITCRL 64

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OY      61 AVSIEQYGLNENNVGVCSENNINFPVLAALYLGIIPVATSNDMYTGDGELTGHLSKP    120  
| :: : | : ||| | ||| | : | : || | | : ::  
DB      65 AEAMKNEGMKPEEHIALCSENCSEEFIPVLAGLYIGVAVAPINEITYTLRELNHSLGTAQP    124

```
Oy      121 TIMSSKALPLILRVQONLSFIKKVVVIDSMYDINGVECVSTFVARYTDTHTFDPLSEFTP 180
        ||::|||: ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      125 TIVFSRKGLPKVLEVOKTVTCTIKRTIYLDSKVNFEGHDCMETFIKKHVELGTFQPSSFVP 184
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0y      181 KDF-DPLEKALIMSSSGTGLPKGVVLSHRSLTIRFVHSRDPYGTRTVPQTSILSLVP 239
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      185 IDVKNRKQHYALLMNSSSGTGLPKGVIRITHEGAVTRFESHADPIYGNQVSPGTAILTVLP 244

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Oy      240 FHHAFGMEFTLLSYFVVGLKVVMLKEEGALELKTIONYKIPTIVAPRVMFSLAKSPVD 299  
        ||| ||||| | | : ||| | : ||| : | : : : | : | | | : |  
Db      245 FHNGFGMEFTLLGYFACGYRVVLMTLKFDEELFLRTLQDYKCYSVLVPTLFAILNKSELID 304
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Qy      300 QYDLSLTFEATGAGAPLGGKDVAAEAVAKRLKPGIIQGYGLEETCCAVMITPHNAVKGTST 359
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      305 KFDLSNLTELASGAGAPLAKEVEGEAVARRFNLPGVROGYGLEETTSAFIITPEGDDKPEAS 364

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0y      360 GRPLPYIRAKVLDNATGKALGPERGEICFQSEMIWKGYNNPEATIDTIDKDGWLHSGD 419
      | : : | | : | | | | | | | : : | | | | | : | | : | |
Db      365 GKVPFLKAVVIDDTKKTGLVNRGEICVKGPSLMGLSYNPEATRETIDEEGWLHTGD 424

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Qy	420	IGYYDEDEGNEFFIVDRLEKELIKYKQVAPAELENLLQHPISADAGVGTGVPDEFEGGOLPA	479
		:              :      :           :	
Db	425	IGYYDEDEHFFIVDRLEKSLIKYKQVAPAELESVLLQHPNIFDAGVAGVPPDPDAGELPC	484

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0y 480 ACVLESGKLTLEKEVODFIAAQVPTPKHLRGVGFVDSIPKPGTGLIRKELREIFAQR 539
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 485 AVVVMKEKTMTEKEIVDYVNSQVNVNHHKRLRGVGFVDEVPKGLTGKIDAKVIREIL--K 542

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Qy	540	APKSKL	545
		::  :	
Db	543	KPQAKM	548

RESULT	12	
Q27348		
ID	Q27348	PRELIMINARY; PRT; 548 AA.

DT	DT	DT	DT
01-NOV-1996	(TREMBlrel, 01, Created)	01-NOV-1996	(TREMBlrel, 01, Last sequence update)
01-DEC-2001	(TREMBlrel, 19, Last annotation update)		

05 *Luciola lateralis* (Firefly).  
0C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
0C Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;

OX	NCBI_TaxID=7052;
RN	[1]
RP	SEQUENCE FROM N.A.

RA Cho K.H., Choi Y., Boo K.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]

RP	SEQUENCE FROM N.A.
RC	STRAIN=MJU; TISSUE=ABDOMEN,
RA	Cho K., Chol Y., Boo K.;

RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

DR	EMBL; U49182; AAA91472.1; -	
DR	EMBL; Z49891; CAA90072.1; -	
DR	HSSP; P08659; ILCI.	
DR	InterPro; IPR000873; AMP-bind.	
DR	Pfam; PF00501; AMP-binding; 1.	
DR	PROSITE; PS00455; AMP_BINDING; 1.	
SQ	SEQUENCE 548 AA: 60062 MW: D237F6EC97CA3B8D CRC64:	

Query Match	51.8%;	Score 1457.5;	DB 5;	Length 548;
Best Local Similarity	51.8%;	Pred. No. 3.3e-104;		
Matches 282; Conservative	101;	Mismatches 158;	Indels 3;	Gaps 2;

```
OY      3 EENIRHGERPRDVIHPGSAGQQLYSLYKFSPFE-AIIDAHTNEVISAOIFETSCRLA 61
       :|||:|||:|||:|||:|||:|||:|||:|||
Db      7 DENIVYGPKPEYPIDEGSAGAQLRKMYMDRVAKLGAIATNALTGVDYTYAEVLEKSCCLG 66
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62 VSIEQYGLENNVMVGCSENNINFNPLYALALYLGIPIVATSDMYTDTGELTGLHNLISKPT 121
   :: ||| : : ||| | ||| |::: | | | ||||
67 EALKNYGLVVDGRIALCSENCSEEFIPVLAGLFIGVGVAPTNEIYTLRELVHSLGISKPT 126

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Qy      122 IMSSKKALPEILRVQONLSFIKKVVVIDSMYDINGVECVSTFVARYTDTHTFDPLSTPK 181
        |:||||| | ::||::| | |::| | |::| |
Db      127 IVFSSKKGDLVITVQKTVAIKTIVLIDSKVDYRGYQSMDFIKKNTPPGFKGSSFRKV 186
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Qy      182 DFDPLEKIALIMSSGTTGLPKGVVLSHKSLTIRFVHSRDPITYGRTPVPQTSLSVPEHH    241  
          :   |::|::::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db      187 EVNRKEQVALI MNSSGSTGLPKGVQLTHENAVTRFSHARDPIYGNQVSPTAILTVPEEH    246
```

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QY 242 HAFGMFTTISYFVVGGLKVMLKKKEGALFLKTIQNYKIPITIVAPVPMVELAKSPLYDOY 301
| | | | | | | | : : | | | | : : | : | : | : |
Db 247 HGFGMFTTILGTYLTCGFRIVMLTKFEDETFLKTLQDYKCSSVILVPTLFAILNRSELDKY 306
```

```
QY      302  DLSSLTVEATGAGAPLGKDVAEAAVAKRKLPGLIIQGYGLTECCAVMITPHNAVKTGSTGR 361
      |||:| |:|:|||| |:|: |||:| |||:| |||:| |:|:|
Db      307  DLSNLVEIASGAPLSKEIGEAVARRNLPVGRQGYGLTETISAILITPEGDDKPGASGK 366
```

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QY      362  PLPYIKAVLDNATGKALGPGERGEICFQSEMIWKGYNNPEATIDTIDKDGWLHSGDIG 421
      :  |  ||||:  |  |  ||  ||||:  |  ||||:  ||||:  ||||:  ||||:  ||||
Db      367  VVPLFKAKAVLDLDTKKTTLGPNRRGEVCVKGPMMLMGVYDNPETREIIDEEGWLHTGSDIG 426

```

```
QY 422 YYDEDCNEFFYDLRKELIKYKGYQVAPAELENLLQHPISADAGVTGVPDEFEGGOLPAAC 481
    |||: ||||| ||||| |||: |||: ||| ||| |
Db 427 YYDEEKHEFFYDLRKSLIKYKGYQVPAELESVLLQHPNIFAGVAGVPPDIAGELPGAV 486
```

```
OY      482 VVLESGKTTEKEVÖDFAAQVTPYTKHRLRGGVFVDSIPKGPYGLIRKELREIFAQBP 541
        ||| |::||| |::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      487 VVLEKGKSMEKEVM DYVAGOVSNARKLRGGRVFDEVPKGLTGKIDGAIRTEL--KKP 544
```

QY	542 KSKL	545
	:1:	
Db	545 VAKM	548

RESULT 13	
Q27757	
ID Q27757	PRELIMINARY; PRT; 545 AA

DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)

05 *Photuris pennsylvanica*.  
0C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
0C Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;

OX	NCBI_TaxID=41716;
RN	[1]
RP	SEQUENCE FROM N.A.

RC TISSUE=LANTERN;  
RX MEDLINE=97307756; Pubmed=9165098;  
RA Ye L., Buck L.M., Schaeffer H.J., Leach F.R.;

Page 7

```

RT "Cloning and sequencing of a cDNA for firefly luciferase from Photuris
RT pennsylvanica.";
RL Biochim. Biophys. Acta 1339:39-52(1997).
CC -1- FUNCTION: PRODUCES GREEN LIGHT WITH A WAVELENGTH OF 562 NM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: PHOTINUS LUCIFERIN + O(2) + ATP = OXIDIZED
CC PHOTINUS LUCIFERIN + CO(2) + H(2)O + AMP + DIPHOSPHATE + LIGHT.
CC -1- COFACTOR: REQUIRES A MAGNESIUM ION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR EMBL; U31240; AAB60897.1; -.
DR HSSP; P08659; 1LC1.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; UNKNOWN_1.
KW Oxidoreductase; Monooxygenase; Photoprotein; Luminescence; Magnesium;
KW Peroxisome.
FT SITE 543 545 MICROBODY TARGETING SIGNAL (POTENTIAL).
SQ SEQUENCE 545 AA; 60649 MW; F0FE4E828047C26E CRC64;

```

Query Match	51.7%;	Score 1454;	DB 5;	Length 545;
Best Local Similarity	50.1%;	Pred. No. 6.2e-104;		
Matches 274;	Conservative 111;	Mismatches 158;	Indels 4;	Gaps 2;

```

Oy 1 MEEENIRHGERPRDIVHPGSAGQOLYSLYKFASPE--AIIDAHTNEVSYAQIFETSC 58
    ||::||:| |::||::||:|::||:|::||:|::||:|::||:|::||:|::||:|
Db 1 MEDKNILYGPPEFHPPLADGTAGEQMFALSKRYADISGCIALTNAHTKENVLYEEFLKLS 60

```

```
QY      59 RLAVSIEOYGINENNVMVGVCSENNINFENPVLAALYLGIPATSNDMYTGDGLTGHNTS 118
       ||| | :||| :| : |||| : || ::||||| | :| | :||
Db      61 RLAESEFKKYLKONDTIAVCSENGLFFLPILASLYLGIITAPVSDKYIERELIHSLGIV 120
```

Qy 119 KPTIMFSSKALPLILRVQÖNL.SFIKWVVIDSMYDINGVECVSTFEVARYTDHTFDPLSE 178  
|||::| :||: |::: ::| |::|::: |||  
Db 121 KPRIIFCSKNTPÖKVLVNKSCLKAYETIIILLDLNEDLGGYÖCINNFISÖNSDINLDVKKF 180

```
QY      179 TPKDFDPLEKIALIMSSSGTTGLPKGVVLSHRSLTIRFVHSRDPITYGTRTVPQTSLSLV 238  
        | : ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db      181 KPNSFNRRDOVALVMFSSSGTGTGSCKGYMLTHKNIVARESHCKDPFGNAINPTTALLTYI 240
```

```
QY      239 PFHNAFGMFTLLSYFVVLGLKVVMMLKKEGALLFKTIONYKRIPTIVAVRPVMVFLAKSPV 298
      |||| ||| ||| || : : : || |||:::|||| : : : || || ||
Db      241 PFHNGFGMTTLGYPFCGFRVALMHTHEEKLFLQSLQDYKVESTLLVPTIMAFEPKSAIV 3000
```

QY      299 DQYDLSLIEVATGCGAPLGKDVAAEAVAKRLKLPGLIIGYGLETETCCAMITPHNAVKTGS 358  
:::||||| :||| ||| | : ||||| ||| ||| : ||  
Db      301 EKYDLSHLEEIASGGAPLSKEIGENWKKREKLNFVRGGYSTETTSAVLITPDTDVRRPS 360

QY 359 TGRPLPIITAKVLDNATGKALPGERGEICFOSEMIMKGYNNPEATIDTIDKGWLSHG 418  
|| : || | || | || | : : || || || || || | : || || ||  
Db 361 TGRIIVPFAHVKKVDDPTGKTIIPNENGEL YFKGDMMKSYVNNEEATKATITNKDGL BSC 420

[illegible]

QY 479 AACVLESGKLTTEKEVODFIAAOVTPTKHLRGVWFVDSTPKPTGKLIRKELREIFAQ 538  
db 481 AAGVVAVGTGKYVTNEOTIVONEVSQVSMATKI PSCVKET LDTTDCGCMGRDVRU DPMWY E40

QY	539	RAPKSKL	545
Ob	541	u--kswt	545

## RESULT 14

ID	Q27321	PRELIMINARY;	PRT;	548 AA.
AC	Q27321;			
DT	01-NOV-1996	(TREMBlrel, 01, Created)		
DT	01-NOV-1996	(TREMBlrel, 01, Last sequence update)		

```

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE LUCIFERASE.
OS Luciola lateralis (Firefly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Elateriformia; Cantharoidea; Lampyridae; Luciola.
OX NCBI_TaxId=7052;
RN [11]
RP SEQUENCE FROM N.A.
RA Cho K., Choi Y., Boo K.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases
RN [12]
RP SEQUENCE FROM N.A.
RA STRAIN=MUJU; TISSUE=ABDOMEN;
RC Cho K.H., Choi Y., Boo K.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=MUJU; TISSUE=ABDOMEN;
RA Cho K., Choi Y., Boo K.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z69619; CAA93444.1; -.
DR EMBL; U49181; AAA91471.1; -.
DR EMBL; U51019; AAB00229.1; -.
DR HSSP; P08659; 1LC1.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 548 AA; 60048 MW; E26CEC26F423E5E8 CRC64;

```

Query Match	51.7%;	Score 1453.5;	DB 5;	Length 548;
Best Local Similarity	51.7%;	Pred. No. 6.8e-104;		
Matches 281;	Conservative 102;	Mismatches 158;	Indels 3;	Gaps 2

```
QY      3 EENIRGERPRDIVHPSAGQQLYQSLYKFASPE-AIDAHTNEVISYAQIFFTSCRLA 61
       :||| :| :| : |||| || : : :| | :| :| :||| :||| |
Db      7 DENIVYGPKFPYPPIEESGAGAQLRKMYMDRYAKLGATAFTNALTGVDITYAEYLEESCCLG 66
```

```
QY      62 VSIEQYGLNENNVAVCSENNINFEFNPVLAALYLGIPVATSDMYTDGELTGHLNISKPT 12
      :: ||| : : |||| | |||| : :: : || : || : || || || ||
Db      67 EALKNYGLVVDGRIALCSENCFFIIPVLAGLFYGVAPTNEIYTLRELVHSLGISKPT 12
```

QY 122 IMFSSKALPLIRVOQNLSFIKKVVIDSMYDINGVECVSTFEVARYTDHTFDPLSFTPK 18  
|:||||| | ::||:: ||:||:| | : : | : |  
Db 127 IVFSSKGGLDKVITVOKTVAIKTIIVILDSKVDRGYOSMDNFIKNTPPGFGKSSFKTV 18

**QY**      182 DFDPLEKIALIMSSGGTGLPKGVLSHRSLTIRFVHSRDPITYGTRTPQTSLSPFH 24  
       : :::::|||||: || |::::|||  
**Dd**    187 EVNRKEOVALINSSSGTGLPKGVOLTHENAVTRSHARDPIGNOSPGTAILVPFH 24  
  :

QY 242 HAFGEMTTLSFYVVGGLKVMMLKKFEGALFKTIONKYIPTIVAPVPMVELAKSPLDQY 30  
| | | | | : : : | : : : | : : : | : : : | : : : |  
Db 247 HGFGEMTTTGYLTGGFTVMTKEDEETFKTLDYKCSSVTI.VPTL.FAII.NRSEFLDKRY 30

0Y 302 DLSLLEVATGCGAPICGDVAEAVAKRLKLPGLIOGYLETTCCAVMITPHNAVKTGSTGR 36  
 307 DI SMI VETASGCGAPISKEITGEFAVABRPNT PCVPOCGCI TETTTSAITTEPFCDNRCPASGK 36

[illegible]

```

QY      422  YDDEDEGNEFFIVDRLEKELIKYKGQVAPAELENNLLQHPISADAGVTGPDPDEFGLLPAC 48
         |||| : ||||| ||||| ||||| : ||||| : ||| |||| 1: |||
05      427  YDEDEKRENTVDIKKCI TEKKVCQVNDRI TEQVLCQNDRIIDQVQVYDDEDEKELIPAC 48

```

[illegible]

QY 542 KSKL 545  
:|:

DB 545 VAKM 548

RESULT 15

09VCC6

ID 09VCC6 PRELIMINARY; PRT: 544 AA.

AC 09VCC6;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CG6178 PROTEIN (GM05240P).

GN CG6178.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Held G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferltera S., Fleischmann W.,

RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003746; AAF56245.1; -

DR EMBL; AY060906; AAL28454.1; -

DR HSSP; P08659; 1IC1.

DR FlyBase; FBgn0039156; CG6178.

DR InterPro; IPR000873; AMP-bind.

DR Pfam; PF00501; AMP-binding; 1.

DR PROSITE; PS00455; AMP\_BINDING; 1.

SQ SEQUENCE 544 AA; 59938 MW; E28B8DADCC988F3C CRC64;

Query Match 36.6%; Score 1030; DB 5; Length 544;

Best Local Similarity 41.3%; Pred. No. 3.7e-71;

Matches 230; Conservative 102; Mismatches 183; Indels 42; Gaps 10;

QY 12 PRDIVHPG-----SAGQQLQSLYKFASPE-AIIDAHTNEVISYAQIFETSC 58

DB 7 PGNIYVGGPYTERQAQDSRSIGYI--LDKYSFGDRFVLDVAVNGVEYSASFHKSIY 63

QY 59 RLAVSIEQYGLNENNVGVCSENNINFNPLVALYLGIPIVATSNDMTDGLTGHNIS 118

DB 64 RLAYILQKLGVRQNDVGLSSSENSVNFALMAFAGLAVGATVAPLNTYSDREVDAINLS 123

QY 119 KPTIMFSSKKALPLILRVQONLSFIKKVVID-----SMYDINGVECVSTFVARTDH 171

DB 124 KPKIIFASKITIDRVAVAKVASKNKFVKGIILSGTSKKFKNIYDLKL-----MEDE 174

QY 172 TFDPL-SETPKDFDPLEKIALIMSSGTTGLPKGVLSHRSLSRTIRFVHSRDPITGRTVP 230

DB 175 KEKTPDFTSPANKDEDVSLIVCSSGTTGLPKGVQLTOMNLATLDSQIQP---TVIP 230

QY 231 --QTSILSLVPHFAFGMFTLSYFVGLKVMKKFEGALFKTIQNKIPTIVVAPV 288

DB 231 MEEVTLTVIPMFHAFGCLTLTTACVGARLVYLPKFEKFLPSAIEKYRVMAFVPP 290

QY 289 MFLAKSPLYVDYDLSLSTEATGAPLGKDVAAVAKRLKPLGIQGYGLTETCAVMI 348

DB 291 MFLAKHPYVDKDLSSLVLLCGAAPLSRETEQIKERIGVPEIRQGYGLSESTLSVIV 350

QY 349 TPHNAVKTGSTGRPLPIKAKVLNATGKALGPERGEICFQSEMIMKGYNNPEATIDT 408

DB 351 QNDEFCKPGSVGLKVIYAKVIDPDTGKLLGANERGELCFKGDGIMKGYIGDTKST-QT 409

QY 409 IDKDGWLHSGDIGYDEDEGNFTIVDRKLKIKYGYQVAPAELENLLQHPSIADAGVTG 468

DB 410 AIKDGWLHTGIDIGYDDDEFFIVDRIKELIKYGYQVPAEIALLLTNDKIKDAVIG 469

QY 469 VPDEFGQLPACVVLSEKTLTEKEVDFIAAQVPTKHLRGVVFVDSIPKPTGKLI 528

DB 470 KPDEEAGELPLAFVVKQANVQLTENEYIQFVNDNASPAKRLRGVIVFVDEIPKPSGKIL 529

QY 529 RKLREIFAQRAPKSL 545

DB 530 RILREMLKKQ--KSKL 544

Search completed: September 4, 2002, 15:07:47

Job time: 246 sec

